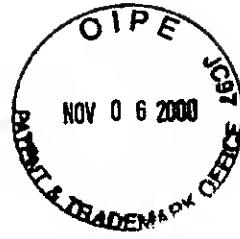


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<110> Fujii, Ryo  
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Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg  
35 40 45  
Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Pro Gly Asp Gly Pro  
50 55 60  
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly  
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Gln Glu

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TGGTACGCRG GCGGTGGGAT CCGGCCCCGTG GGCGCGTTCG GCCGGCGAAG AGCTGCCCYG 180  
GGGGACGGAC CCAGGGCTGG CCCCCGGCGT GTGCCGGCCT GCTTCCGCCT GGAAGGCGGY 240  
GCTGAGCCCT CCCGAGCCCT CCCGGGGCGG CTGACGGCCC AGCTGGTCCA GGAA 294

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<213> Bovine

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<211> 31

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<213> Bovine

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<212> PRT

<213> Bovine

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<212> PRT

<213> Bovine

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Arg

33

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<211> 20

<212> PRT

<213> Bovine

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<211> 21

<212> PRT

<213> Bovine

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Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro  
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<210> 10

<211> 22  
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Val Gly Arg Phe Gly Arg  
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<211> 60

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<211> 63

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<211> 66

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GGCGG 66

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<211> 91  
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Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala  
20 25 30  
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val  
35 40 45  
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr  
50 55 60  
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr  
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Val Val Leu Val His Pro Leu Arg Arg Arg Ile  
85 90

<210> 20  
<211> 59  
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<400> 20

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu  
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20 25 30  
Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg  
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Thr Phe Cys Leu Leu Val Val Val Val Val Val Val  
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<210> 21  
<211> 370  
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<213> Human  
<400> 21

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Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala  
20 25 30  
Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr  
35 40 45  
Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val  
50 55 60  
Leu Leu Tyr Ser Val Val Val Val Gly Leu Val Gly Asn Cys Leu  
65 70 75 80  
Leu Val Leu Val Ile Ala Arg Val Arg Arg His Asn Val Thr Asn

	85	90	95
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala			
100	105	110	
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val			
115	120	125	
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr			
130	135	140	
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr			
145	150	155	160
Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser			
165	170	175	
Ala Tyr Ala Val Leu Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu			
180	185	190	
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val			
195	200	205	
Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu			
210	215	220	
Tyr Ala Trp Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val			
225	230	235	240
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val			
245	250	255	
Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg			
260	265	270	
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala			
275	280	285	
Val Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp			
290	295	300	
Pro His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys			
305	310	315	320
His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala			
325	330	335	
Trp Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala			
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355	360	365	
Val Ile			
370			

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<211>	206
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<213>	Murine
<400>	22

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Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
			20					25				30			
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
			35				40				45				
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Ala	Val	Thr
				50			55				60				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
	65				70				75				80		
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser
				85				90				95			
Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp	Val	Leu	Ser	Ala	Val	Leu	Ala	Leu
				100				105				110			
Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val
				115				120				125			
Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu

130 135 140  
Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val  
145 150 155 160  
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val  
165 170 175  
Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg  
180 185 190  
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val  
195 200 205

<210> 23

<211> 126

<212> PRT

<213> Murine

<400> 23

Val Val Leu Val His Pro Leu Arg Arg Ile Ser Leu Arg Leu Ser  
1 5 10 15  
Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu  
20 25 30  
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val  
35 40 45  
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile  
50 55 60  
Tyr Ala Trp Gly Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala  
65 70 75 80  
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val  
85 90 95  
Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg  
100 105 110  
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val  
115 120 125

<210> 24

<211> 273

<212> DNA

<213> Human

<400> 24

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAAACG TGACGAACCT CCTCATCGGC 60  
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GCCTTCCAGC CACGCGGCTG GGTGTTCCGGC GGCGGGCTGT GCCACCTGGT CTTCTTCCCTG 180  
CAGCCGGTCA CCGTCTATGT GTCGGTGTTAC ACGCTCACCA CCATCGCAGT GGACCCGGTAC 240  
GTCTTGCTGG TGCACCCGCT CAGGGCGCGC ATC 273

<210> 25

<211> 177

<212> DNA

<213> Human

<400> 25

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GTGTCACTGA	AGCTCCGAA	CCCGCGTGGTG	CCGGGCTGCG	TGACCCAGAG	CCAGGCCGAC	120
TGGGACCGCG	CTCGGCGCCG	GCGCACCTTC	TGCTTGTGG	TGGTGGTCTG	GGTGGTG	177

<210> 26

<211> 1110

<212> DNA

<213> Human

<400> 26

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GGCGCGGAGC	CTCCAGCCGT	CGGGCCCTTC	CAGAGCCTGC	AGCTGGTGCA	TCAGCTGAAG	180
GGGCTGATCG	TGCTGCTCTA	CAAGCGTCGTG	GTGGTGGTGG	GGCTGGTGGG	CAACTGCTG	240
CTGCTGCTGG	TGATCGCGCG	GGTACCGCCGG	CTGCACAAACG	TGACCAACTT	CCTCATCGGC	300
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCCG	TGCCGCTCAC	GCTGGCCATAT	360
GCCTTCGAGC	CAACGCGCTG	GGTGTTCGGC	GGCGGCCCTGT	GCCACCTGGT	CTTCTTCCCTG	420
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTC	ACGCTCACCA	CCATCGGAGT	GGACCGCTAC	480
GTCGTGCTGG	TGGACCCGCT	GAGGCGGCCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	540
CTGGCCATCT	GGGCGCTGTC	CCGGCTGCTG	GCGCTGCCCG	CCGCCGTTGCA	CACCTATCAC	600
GTCGGAGCTCA	AGCCGACCGA	CGTGGCCCTC	TGGCAGGAGT	TCTGGGGCTC	CCAGGAGCCG	660
CAGGCCAGC	TCTACGCCCTG	GGGGCTGCTG	GTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	720
ATCCTCCCTGT	CTTACGTCCG	GGTGTCACTG	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCTGC	780
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGGCGC	GGGCACCTT	CTGCTTGTG	840
GTGGTGGTCTG	TGGTGGTGTGTT	CCGGCTCTGC	TGGGTGCCGC	TGCACGTCTT	CAACCTGCTG	900
CGGGACCTCG	ACCCCCAGGC	CATCGACCCCT	TACGCCCTTG	GGCTGGTGC	GCTGCTCTGC	960
CACTGGCTCG	CCATGAGTTC	GGCCTGCTAC	AACCCCTTCA	TCTACGCCCTG	GCTGCACGAC	1020
AGCTTCGGCG	AGGAGCTGCG	CAAACGTGTTG	GTCGCTTGGC	CCCGCAAGAT	AGCCCCCAT	1080
GGCCACAATA	TGACCGTCAG	CGTGGTCATC				1110

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<211> 618

<212> DNA

<213> Murine

<400> 27

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GCCTTCGAGC	CAACGCGCTG	GGTGTTCGGC	GGCGGCCCTGT	GCCACCTGGT	CTTCTTCCCTG	180
CAGGCGGTCA	CCGTCTATGT	GTCGGTGTTC	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	240
GTCGTGCTGG	TGCACCCCGT	GAGGCGGCCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	300
CTGGCCCATCT	GGGTGCTGTC	CCGGGTGCTG	GCGCTGCCCG	CCGGCGTGCA	CACCTATCAC	360
GTGGAGCTCA	AGCCGACGA	CGTGCCTC	TGGCAGGAGT	TCTGGGGCTC	CCAGGAGCCG	420
CAGGCCAGC	TCTACGCCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	480
ATCCTCCCTGT	CTTAGGCCCCG	GCTGTCACTG	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCCGC	540
GTGACCCAGA	CCCAGGCCGA	CTGGGACCGC	GCTCGGGCGC	GGCGGACCTT	CTGCTTGTG	600
GTGCTGGTCTG	TGGTGGTG					618

<210> 28

<211> 378

<212> DNA

<213> Murine

<400> 28

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GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180  
CAACGCCAGA TCTACCCCTG GGGGCTGCCTT CTGGGCACCT ATTGCTCCC CCTGCTGCC 240  
ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGGTGGT GCCTGGCAGC 300  
GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG 360  
GTGGTGGTGG TGGTAGTG 378

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<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 29

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<210> 30

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

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<210> 31

<211> 27

<212> DNA

<213> Unknown

<220>

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<400> 31

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<212> DNA  
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<210> 33  
<211> 24  
<212> DNA  
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*On b  
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b N*  
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<211> 24  
<212> DNA  
<213> Unknown  
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<223> Unsure  
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24

<210> 35  
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<212> DNA  
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<223> Unsure

<400> 35

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<212> DNA

<213> Unknown

<220>

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<210> 37

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<212> DNA

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<212> DNA

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<220>

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<400> 38

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<210> 39

<211> 28

<212> DNA  
<213> Unknown  
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<223> Unsure  
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<210> 41  
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<212> DNA  
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<211> 98  
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20 25 30  
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg  
35 40 45  
Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Leu Gly Asp Gly Pro  
50 55 60  
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly  
65 70 75 80  
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val  
85 90 95  
Gln Glu

*BB  
Bar*

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<211> 83  
<212> PRT  
<213> Rat  
<400> 45

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20 25 30  
Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
35 40 45  
Val Gly Arg Phe Gly Arg Arg Ala Thr Pro Arg Asp Val Thr Gly  
50 55 60  
Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp Gly Arg Thr Lys Phe Ser  
65 70 75 80  
Gln Arg Gly

<210> 46  
<211> 249  
<212> DNA  
<213> Rat  
<400> 46

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TACACGGGCC CGGGGATCAG GCCTGTGGC CGCTTCGGCA GGAGAAGGGC AACCCCGAGG 180  
GATGTCACTG GACTTGGCCA ACTCAGCTGC CTCCCACCTGG ATGGACGCAC CAAGTTCTCT 240  
CAGCGTGGAA 249

<210> 47  
<211> 31  
<212> PRT  
<213> Rat  
<400> 47

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn  
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Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe  
20 25 30

<210> 48  
<211> 32  
<212> PRT  
<213> Rat  
<400> 48

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn  
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Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly  
20 25 30

<210> 49  
<211> 33  
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<213> Rat  
<400> 49

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn  
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Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly

Arg 20

25

30

<210> 50

<211> 20

<212> PRT

<213> Rat

<400> 50

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
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Val Gly Arg Phe  
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<210> 51

<211> 21

<212> PRT

<213> Rat

<400> 51

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Gly  
20

*AB* <210> 52

*AB* <211> 22

*AB* <212> PRT

*AB* <213> Rat

*AB* <400> 52

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro  
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Val Gly Arg Phe Gly Arg  
20

<210> 53

<211> 93

<212> DNA

<213> Rat

<400> 53

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ACGGGCGCGC GGATCAGGCC TGTGGGCCGC TTC

93

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<212> DNA  
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ACGGGCGCGC GGATCAGGCC TGTGGGCCGC TTCGGC 96

<210> 55  
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<212> DNA  
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ACGGGCGCGC GGATCAGGCC TGTGGGCCGC TTCGGCAGG 99

*AB*  
*AB*  
*AB*  
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<211> 60  
<212> DNA  
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<211> 63  
<212> DNA  
<213> Rat  
<400> 57

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGGGGGA TCAGGCCTGT GGGCCGCTTC 60  
GGC 63

<210> 58  
<211> 66

<212> DNA

<213> Rat

<400> 58

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGGGGA TCAGGCCTGT GGGCCGCTTC 60  
GGCAGG 66

<210> 59

<211> 87

<212> PRT

<213> Human

<400> 59

Met Lys Val Leu Arg Ala Trp Leu Leu Cys Leu Leu Met Leu Gly Leu  
1 5 10 15  
Ala Leu Arg Gly Ala Ala Ser Arg Thr His Arg His Ser Met Glu Ile  
20 25 30  
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg  
35 40 45  
Pro Val Gly Arg Phe Gly Arg Arg Ala Thr Leu Gly Asp Val Pro  
50 55 60  
Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys Phe Pro Leu Glu Gly Gly  
65 70 75 80  
Ala Met Ser Ser Gln Asp Gly  
85

*ABK*  
<210> 60

<211> 261

<212> DNA

<213> Human

<400> 60

ATGAAGGTGC TGAGGGCCTG CCTCCCTGTGC CTGCTGATGC TGGGCCTGGC CCTGGGGGA 60  
GCTGCAAGTC GTACCCATCG GCACTCCATG GAGATCCGCA CCCCTGACAT CAATCCTGCC 120  
TGGTACGCCA GTCGCGGGAT CAGGCCTGTG GGCCGCTTCG GTGGAGGAG GGCAACCTG 180  
GGGGACGTCC CCAAGCCTGG CCTGCGACCC CGGCTGACCT GCTTCCCCCT GGAAGGGGT 240  
GCTATGTCGT CCCAGGATGG C 261

<210> 61

<211> 31

<212> PRT

<213> Human

<400> 61

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
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Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe

20

25

30

<210> 62

<211> 32

<212> PRT

<213> Human

<400> 62

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly  
20 25 30

<210> 63

<211> 33

<212> PRT

<213> Human

<400> 63

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
1 5 10 15  
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly  
20 25 30

Arg

*Arg*  
<210> 64

<211> 20

<212> PRT

<213> Human

<400> 64

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe  
20

<210> 65

<211> 21

<212> PRT

<213> Human

<400> 65

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro

1 Val Gly Arg Phe Gly 5  
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10

15

<210> 66

<211> 22

<212> PRT

<213> Human

<400> 66

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Gly Arg  
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<210> 67

<211> 93

<212> DNA

<213> Human

<400> 67

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GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTC 93

*AB*  
*AB*  
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<210> 68

<211> 96

<212> DNA

<213> Human

<400> 68

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60  
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGT 96

<210> 69

<211> 99

<212> DNA

<213> Human

<400> 69

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60  
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGT 99

<210> 70  
<211> 60  
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<400> 70

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60

<210> 71  
<211> 63  
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<400> 71

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60  
GGT 63

<210> 72  
<211> 66  
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ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60  
GGTCGG 66

<210> 73  
<211> 21  
<212> PRT  
<213> Unknown  
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Xaa of the 11th position is Gly or Ser.  
Xaa of the 21st position is H, Gly or GlyArg.  
<400> 73

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Xaa Arg Gly Ile Arg Pro  
1 5 10 15  
Val Gly Arg Phe Xaa  
20

<210> 74  
<211> 11  
<212> PRT  
<213> Unknown

<220>  
<223> Unsure. Xaa of the 3rd position is Ala or Thr.  
Xaa of the 5th position is Gln or Arg.  
Xaa of the 10th position is Ile or Thr.

<400> 74

Ser Arg Xaa His Xaa His Ser Met Glu Xaa Arg  
1 5 10

<210> 75  
<211> 26  
<212> DNA  
<213> Unknown  
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<223> Unsure  
<400> 75

CARCAYTCCA TGGAGACAAG AACCCC 26

*Part B*  
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<212> DNA  
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<400> 76

TACCAGGCAG GATTGATACA GGGG 24

<210> 77  
<211> 25  
<212> DNA  
<213> Unknown  
<220>

<228> Unsure

<400> 77

GGCATCATCC AGGAAGACGG AGCAT 25

<210> 78

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 78

AGCAGAGGAG AGGGAGGGTA GAGGA 25

<210> 79

<211> 22

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 79

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*ABW*  
<210> 80

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 80

GCCTGATCCC GCGGCCCGTG TACCA 25

<210> 81

<211> 26

<212> DNA  
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<400> 81

TTGCCCTTCT CCTGCCCAAG CGGGCC 26

<210> 82  
<211> 27  
<212> DNA  
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<400> 82

GGCGGGGGCT GCAAGTCGTA CCCATCG 27

<210> 83  
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CGGCACTCCA TGGAGATCCG CACCCCT 27

<210> 84  
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<212> DNA  
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<223> Unsure  
<400> 84

CAGGCAGGAT TGATGTCAGG GGTGCGG 27

<210> 85  
<211> 27  
<212> DNA  
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<223> Unsure  
<400> 85

CATGGAGTGC CGATGGTAC GACTTGC 27

<210> 86  
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GGCCTCCTCG GAGGAGCCAA GGGATGA 27

*AB*  
<210> 87  
<211> 27  
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<223> Unsure  
<400> 87

GGGAAAGGAG CCCGAAGGAG AGGAGAG 27

<210> 88  
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<212> DNA  
<213> Unknown  
<220>  
<223> Unsure

<400> 88

CCTGGTGGCC ATTCTCCTGT CTTAC 25

<210> 89

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 89

GGGTCCAGGT CCCGCAGAAG GTTGA 25

<210> 90

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 90

GAAGACGGAG CATGGCCCTG AAGAC 25

*ABW*  
<210> 91

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 91

GGCAGCTCAG TTGGCCAAGT CCAGT 25

<210> 92

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 92

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Cys  
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<210> 93

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 93

Cys Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe  
1 5 10 15

<210> 94

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 94

Cys Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly  
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<210> 95

<211> 30

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 95

AGATTGGCAT CATCCAGGAA GACGGAGCAT 30

<210> 96  
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<212> DNA  
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<400> 96

GCTGACTCGA CAGCACTGTC TTCTCGAGCT G 31

<210> 97  
<211> 21  
<212> DNA  
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<220>  
<223> Unsure  
<400> 97

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*BL*  
*CK*  
AACCCCTTCA TCTATGCGTG G 21

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<211> 20  
<212> DNA  
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<223> Unsure  
<400> 98

ATATTCTGGC CATGAGGCAC 20

<210> 99  
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<212> DNA  
<213> Unknown  
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<223> Unsure

<400> 99

TTCCGAGAGG AGCTACGCAA GATGCTTC 28

Prob  
B1  
Bnk